



841 SFARTVNKEYPGLADPVFRTLVSQILDQAEPLSSLSSEVVTVFOYYSYFTSHGVSDLE 900
901 SYLSQLARQVSMVQTLQSLRDEKLLQTMSDLAPSNLLAQQEVLRTLALLLTREDNEVSEA 960
961 VTLYLAAASKNQHFREKALLYCEALTTKTNLQLQKAACIALKILEATESIKMLVTLCOQSD 1020
1021 TEEIRNVASETLLSLGEDGRLAYEQLDKFPRDCVKVGGRHGTEVATAF 1068

Top sequence: predicted Diff40 long form (BAA20840) (SEQ ID NO:37)
Bottom sequence: predicted Diff40 short form NCBI (NP_056948) (SEQ ID NO:38)

FIG. 6C

[illegible]

Top sequence: predicted Diff40 long form (BAA20840) (SEQ ID NO: 39)
Bottom sequence: T2DM-1a (SEQ ID NO: 2)

FIG. 7C

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3358 FFSNLPDDIFENGKAAEEKMPLSLSFSDLPNGDCALTSHSTGSPSNSTNPEITITPAEF. 416
      : | | . | . | | . | | . | | . | | . | | . | | . | | . | | . | |
3357 YLSVL.....QQPTQQA...LLGGPRATSILSYLSDSDLRGPSLRQSQE L P 401
      .
4417 NLSSLASQNEGMDDTSSASSRNSLG...EGQEPKSHLKEEDPEEPRKPASAPSEACRRQS 473
      : | . |: . : || ... | . . | | . : . | | . : | | . | | . | | . | |
4402 EMDSFSSDPPRD TETSTASTSDVGFLPLTFGPHASIEEEAREDP L PPGLPEMA..HLS 459
      .
4474 SGAGAE 479
      | | |
4460 GGPFAEQPGWRNLGGESPSLPQGSLFHSGTASSSQNGHEEGATGDREDGPGVALEGPLQE 519
      .
5520 VLELLRP TD STQPQLRELEYQV LGFRDR LKVWPPRPGRWPFCFADGMTTGS R GLWGHA AWA 579
      .
5580 DILASPLRDLGGPC LSGPWFFPHLASGDNNSPHG AQ E DFKSSQ 621

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Top sequence: predicted Diff40 Short form (RefSeq NP_056948) (SEQ ID NO: 40)
Bottom sequence: T2DM-1b (SEQ ID NO: 4)

F/G/B

841 SFARTVNKEYPGLADPVFRTLVSQILDQAEPLLSLSSSEVTVFQYYSYFTSHGVSDLE 900
 901 SYLSQLARQVSMVQTLQSLRDEKLLQTMSDLAPSNLLAQQEVLRTLALLLTREDNEVSEA 960
 961 VTLYLAASKNQHFREKALLYCEALTKTNLQLOKAAACLALKILEATESIKMLVTLQCSD 1020
 1021 TEEIRNVASETLLSLGEDGRLAYEQLDKFPRDCVKVGGRHGTAVATAF 1068

Top sequence: predicted Diff40 long form (BAA20840) (SEQ ID NO: ~~23~~37)
 Bottom sequence: predicted Diff40 short form NCBI (NP_056948) (SEQ ID
 NO: ~~24~~38)

FIG. 6C

710 RGHLSALETDTGVGTSVAGSPLPLTTGNESLDITIVRHLQYCTQLVQQIVFSSKTPFVA 769
 602SSLKASSRELTAGAPELDVLLMVHLQVCKALLQKLASPNLSRLVQ 646
 770 RSLLEKLSRQIQVMEKLAASVDENIGNISSVVEAIPFHKKLSLFSWTKCCSPVGVIHS 829
 647 ECLLEEVAQQKHVLETLVLDFEKVGKATSIIEEIPQASRTKGCLKLWRGCTGPGRVLSC 706
 7
 830 PADRVMKQLEASFARTVNKEYPGLADPVFRTLVSQILDQAEPLLSLSSSE.VVTVFQYY 888
 707 PATLLNQKKTFQHRVRGKYPGQLEIACRRLLQVSCGGLPGAGLPCEEQIITWFOFH 766
 889 SYFTSHGVSDLESYLSQARQVSMVQTLQSLRDEKLLQTMSDLAPSNLLAQQEVRLTAL 948
 767 SYIQRQSVSDLEKHFQTLTKEVTLIEELHCAGQAKVVRKLGKRLGQLQPLPQTLRAWAL 826
 949 LLTREDNEVSEAVTLYLAAASKNQHFREKALLYCEALTKTNLQKAAACIALKILEATE 1008
 827 LQLDGTPRCRAASARLAGAVRNRSFREKALLFYTNALAENDARLQQAACIALKHLKGIE 886
 1009 SIKMLVTLCQSDTEEIRNVASETLLSLGEDGRLAYEQLDK 1048
 887 SIDQTASLCQSDLEAVRAARETTLSFGEKGRLAFEKMDKLCSEQREVFCEADVEITIF 946

Top sequence: predicted Diff40 long form (BAA20840) (SEQ ID NO: ~~123~~39)
 Bottom sequence: T2DM-1a (SEQ ID NO:2)

FIG. 7C

358 FFSNLPDDIFENGKAAEEKMPLSLFSDLPNGDCALTSHTGSPSNSTNPETITPAEF. 416
:
| |

.....QOPTQQAL..LLGGPRATSILSYLSDSDLRGPSLRSSQSQELP 401
:
| | . | | . | | . | | : |
357 YLSVL..... 401

417 NLSSLASONEGMDDTSSASSRNSLG...EQEPPKSHLKEEDPEEPKPAPASEACRRQS 473
:
| |: :|| ..|. |.: || | | | | |
402 EMDSFSEDPRDTETSTSASTSDVGFLPLTFGPHASIEEEEAREDP LPPGLLEMA..HLS 459

474 SGAGAE 479
| | |
460 GGPF AEQP GWRNLGGESP LPQG SLFHSGT ASSSQNGHEEGATGDREDGPGVALEGPLQE 519

520 VLELLRP TD ST Q PQLRELEYQV LGFRDRLKVWPP RPGRWP CFA DGMTGT S RGLWGHA AWA 579

580 D ILA SP LR DL GG PC LS GP WFP PH LA SC DN NSPH GA QE DF K SSQ 621

Top sequence: predicted Diff40 Short form (RefSeq NP_056948) (SEQ ID NO: [24]
40)
Bottom sequence: T2DM-1b (SEQ ID NO: 4)